Express Mail EV 330856466 US
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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of:

HARRIS et al.

Application No.: Not Yet Assigned

Filed: August 4, 2003

For: SCREENING ASSAYS FOR COMPOUNDS THAT CAUSE APOPTOSIS

Customer No.: 20350

Confirmation No.: Not Yet Assigned

Examiner: Not Yet Assigned

Technology Center/Art Unit: Not Yet Assigned

REQUEST TO ACCEPT IN THE PRESENT CASE THE SEQUENCE LISTING FILED IN THE PARENT CASE

Mail Stop Patent Application
Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

Sir:

Applicants have previously filed on October 28, 1996 a sequence listing and accompanying computer readable diskette in the parent Application No. 08/359,316. Applicants request the use of the previously filed diskette containing the sequence information in computer readable form in the parent application in lieu of providing a diskette herewith. The diskette submitted to the USPTO in the parent application on October 28, 1996 is the only computer-readable form filed. The parent application information data is as follows:

Applicants: Harris et al.
Serial No. 08/359,316
Filed: December 19, 1994
Title: SCREENING ASSAYS FOR COMPOUNDS THAT CAUSE APOPTOSIS

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As required by 1.821(f), applicants state that the content of the above-identified computer readable diskette submitted in the parent application is the same as the content of the hard copy of the Sequence Listing (pages 37-43) submitted to the USPTO in the parent application and herewith in the accompanying divisional application.

Respectfully submitted,

Kenneth A. Weber
Reg. No. 31,677

TOWNSEND and TOWNSEND and CREW LLP
Two Embarcadero Center, 8th Floor
San Francisco, California 94111-3834
Tel: 415-576-0200
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Attachments
KAW:dk
60010106 v1

Transmittal Sheet

TOWNSEND and TOWNSEND and CREW LLP
Two Embarcadero Center
Eight Floor
San Francisco, CA 94111-3834
(415) 576-0200
(415) 576-0300 FAX

Atty. Docket No. 15280-225000

Date October 28, 1996

In re application of:

Curtis C. Harris et al.

Serial No.: 08/359,316

Filed: December 19, 1994

Group Art Unit: 1811

For: SCREENING ASSAYS FOR COMPOUNDS THAT CAUSE APOPTOSIS

I hereby certify that this is being deposited with the United States Postal Service as first class mail in an envelope addressed to:
Assistant Commissioner for Patents
Washington, D. C. 20231.

Date: October 28, 1996

Sherry Barton

THE ASSISTANT COMMISSIONER FOR PATENTS
Washington, D.C. 20231

Sir:

Transmitted herewith for the above-identified application are:

[X] Petition to Extend Time [CFR § 1.136(a)] with fee authorization $110.00
[X] Declaration with Exhibits 1-4 [CFR § 1.131]
[X] Amendment [37 CFR § 1.115]
[X] Substitute Paper Copy and Computer Readable Form of Sequence Listing [37 C.F.R. §§ 1.821-1.825]
[X] Fee

[] No fee is due.

Please charge Deposit Account No. 20-1430 as follows:

[X] Any additional fees associated with this paper or during the pendency of this application.

Two copies of this sheet are enclosed.

TOWNSEND and TOWNSEND and CREW LLP

Kenneth A. Weber
Reg. No.: 31,677
Attorneys for Applicants

h:\HOME\JKH\ASP\15280-225.TRN

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: HARRIS, Curtis C.
WANG, Xin Wei
HOEIJMAKERS, Jan H.J.

(ii) TITLE OF INVENTION: SCREENING ASSAYS FOR COMPOUNDS THAT CAUSE APOPTOSIS

(iii) NUMBER OF SEQUENCES: 6

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Townsend and Townsend Khourie and Crew
(B) STREET: Steuart Street Tower, One Market Plaza
(C) CITY: San Francisco
(D) STATE: California
(E) COUNTRY: US
(F) ZIP: 94105-1493

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US not yet designated
(B) FILING DATE: 19-DEC-1994
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Kruse, Norman J.
(B) REGISTRATION NUMBER: 35,235
(C) REFERENCE/DOCKET NO: 15280-225000

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (415) 543-9600
(B) TELEFAX: (415) 543-5043

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 393 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(ix) FEATURE:
(A) NAME/KEY: Protein
(B) LOCATION: 1..393
(D) OTHER INFORMATION: /note= "Amino acid sequence of human wild-type p53."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
Met Glu Glu Pro Gln Ser Asp Pro Ser Val Glu Pro Pro Leu Ser Gln
1               5                  10                  15

Glu Thr Phe Ser Asp Leu Trp Lys Leu Leu Pro Glu Asn Asn Val Leu
            20                  25                  30

Ser Pro Leu Pro Ser Gln Ala Met Asp Asp Leu Met Leu Ser Pro Asp
        35                  40                  45

Asp Ile Glu Gln Trp Phe Thr Glu Asp Pro Gly Pro Asp Glu Ala Pro
    50                  55                  60

Arg Met Pro Glu Ala Ala Pro Arg Val Ala Pro Gly Pro Ala Ala Pro
65                  70                  75                  80

Thr Pro Ala Ala Pro Ala Pro Ala Pro Ser Trp Pro Leu Ser Ser Ser
                85                  90                  95

Val Pro Ser Gln Lys Thr Tyr Gln Gly Ser Tyr Gly Phe Arg Leu Gly
            100                 105                 110

Phe Leu His Ser Gly Thr Ala Lys Ser Val Thr Cys Thr Tyr Ser Pro
        115                 120                 125

Ala Leu Asn Lys Met Phe Cys Gln Leu Ala Lys Thr Cys Pro Val Gln
    130                 135                 140

Leu Trp Val Asp Ser Thr Pro Pro Pro Gly Thr Arg Val Arg Ala Met
145                 150                 155                 160

Ala Ile Tyr Lys Gln Ser Gln His Met Thr Glu Val Val Arg Arg Cys
                165                 170                 175

Pro His His Glu Arg Cys Ser Asp Ser Asp Gly Leu Ala Pro Pro Gln
            180                 185                 190

His Leu Ile Arg Val Glu Gly Asn Leu Arg Val Glu Tyr Leu Asp Asp
        195                 200                 205

Arg Asn Thr Phe Arg His Ser Val Val Val Pro Tyr Glu Pro Pro Glu
    210                 215                 220

Val Gly Ser Asp Cys Thr Thr Ile His Tyr Asn Tyr Met Cys Asn Ser
225                 230                 235                 240

Ser Cys Met Gly Gly Met Asn Arg Arg Pro Ile Leu Thr Ile Ile Thr
                245                 250                 255
```

```
Leu Glu Asp Ser Ser Gly Asn Leu Leu Gly Arg Asn Ser Phe Glu Val
            260                 265                 270

Arg Val Cys Ala Cys Pro Gly Arg Asp Arg Arg Thr Glu Glu Glu Asn
        275                 280                 285

Leu Arg Lys Lys Gly Glu Pro His His Glu Leu Pro Pro Gly Ser Thr
    290                 295                 300

Lys Arg Ala Leu Pro Asn Asn Thr Ser Ser Ser Pro Gln Pro Lys Lys
305                 310                 315                 320

Lys Pro Leu Asp Gly Glu Tyr Phe Thr Leu Gln Ile Arg Gly Arg Glu
                325                 330                 335

Arg Phe Glu Met Phe Arg Glu Leu Asn Glu Ala Leu Glu Leu Lys Asp
            340                 345                 350

Ala Gln Ala Gly Lys Glu Pro Gly Gly Ser Arg Ala His Ser Ser His
        355                 360                 365

Leu Lys Ser Lys Lys Gly Gln Ser Thr Ser Arg His Lys Lys Leu Met
    370                 375                 380

Phe Lys Thr Glu Gly Pro Asp Ser Asp
385                 390
```

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..19
(D) OTHER INFORMATION: /note= "Peptide # p53cp: amino acid sequence of p53 peptide."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
Ser His Leu Lys Ser Lys Lys Gly Gly Ser Thr Ser Arg His Lys Lys
1               5                   10                  15

Leu Met Phe
```

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 781 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(ix) FEATURE:
(A) NAME/KEY: Protein
(B) LOCATION: 1..781
(D) OTHER INFORMATION: /note= "Amino acid sequence of human XPB."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```
Met Gly Lys Arg Asp Arg Ala Asp Arg Asp Lys Lys Lys Ser Arg Lys
1               5                  10                  15

Arg His Tyr Glu Asp Glu Glu Asp Asp Glu Glu Asp Ala Pro Gly Asn
            20                  25                  30

Asp Pro Gln Glu Ala Val Pro Ser Ala Ala Gly Lys Gln Val Asp Glu
        35                  40                  45

Ser Gly Thr Lys Val Asp Glu Tyr Gly Ala Lys Asp Tyr Arg Leu Gln
    50                  55                  60

Met Pro Leu Lys Asp Asp His Thr Ser Arg Pro Leu Trp Val Ala Pro
65                  70                  75                  80

Asp Gly His Ile Phe Leu Glu Ala Phe Ser Pro Val Tyr Lys Tyr Ala
                85                  90                  95

Gln Asp Phe Leu Val Ala Ile Ala Glu Pro Val Cys Arg Pro Thr His
            100                 105                 110

Val His Glu Tyr Lys Leu Thr Ala Tyr Ser Leu Tyr Ala Ala Val Ser
        115                 120                 125

Val Gly Leu Gln Thr Ser Asp Ile Thr Glu Tyr Leu Arg Lys Leu Ser
    130                 135                 140

Lys Thr Gly Val Pro Asp Gly Ile Met Gln Phe Ile Lys Leu Cys Thr
145                 150                 155                 160

Val Ser Tyr Gly Lys Val Lys Leu Val Leu Lys His Asn Arg Tyr Phe
                165                 170                 175

Val Glu Ser Cys His Pro Asp Val Ile Gln His Leu Leu Gln Asp Pro
            180                 185                 190

Val Ile Arg Glu Cys Arg Leu Arg Asn Ser Glu Gly Glu Ala Thr Glu
        195                 200                 205

Leu Ile Thr Glu Thr Phe Thr Ser Lys Ser Ala Ile Ser Lys Thr Ala
    210                 215                 220

Glu Ser Ser Gly Gly Pro Ser Thr Ser Arg Val Thr Asp Pro Gln Gly
225                 230                 235                 240

Lys Ser Asp Ile Pro Met Asp Leu Phe Asp Phe Tyr Glu Gln Met Asp
                245                 250                 255
```

```
Lys Asp Glu Glu Glu Glu Glu Glu Thr Gln Thr Val Ser Phe Glu Val
                260                 265                 270

Lys Gln Glu Met Ile Glu Glu Leu Gln Lys Arg Cys Ile His Leu Glu
        275                 280                 285

Tyr Pro Leu Leu Ala Glu Tyr Asp Phe Arg Asn Asp Ser Val Asn Pro
    290                 295                 300

Asp Ile Asn Ile Asp Leu Lys Pro Thr Ala Val Leu Arg Pro Tyr Gln
305                 310                 315                 320

Glu Lys Ser Leu Arg Lys Met Phe Gly Asn Gly Arg Ala Arg Ser Gly
                325                 330                 335

Val Ile Val Leu Pro Cys Gly Ala Gly Lys Ser Leu Val Gly Val Thr
            340                 345                 350

Ala Ala Cys Thr Val Arg Lys Arg Cys Leu Val Leu Gly Asn Ser Ala
        355                 360                 365

Val Ser Val Glu Gln Trp Lys Ala Gln Phe Lys Met Trp Ser Thr Ile
    370                 375                 380

Asp Asp Ser Gln Ile Cys Arg Phe Thr Ser Asp Ala Lys Asp Lys Pro
385                 390                 395                 400

Ile Gly Cys Ser Val Ala Ile Ser Thr Tyr Ser Met Leu Gly His Thr
                405                 410                 415

Thr Lys Arg Ser Trp Glu Ala Glu Arg Val Met Glu Trp Leu Lys Thr
            420                 425                 430

Gln Glu Trp Gly Leu Met Ile Leu Asp Glu Val His Thr Ile Pro Ala
        435                 440                 445

Lys Met Phe Arg Arg Val Leu Thr Ile Val Gln Ala His Cys Lys Leu
    450                 455                 460

Gly Leu Thr Ala Thr Leu Val Arg Glu Asp Asp Lys Ile Val Asp Leu
465                 470                 475                 480

Asn Phe Leu Ile Gly Pro Lys Leu Tyr Glu Ala Asn Trp Met Glu Leu
                485                 490                 495

Gln Asn Asn Gly Tyr Ile Ala Lys Val Gln Cys Ala Glu Val Trp Cys
            500                 505                 510

Pro Met Ser Pro Glu Phe Tyr Arg Glu Tyr Val Ala Ile Lys Thr Lys
        515                 520                 525

Lys Arg Ile Leu Leu Tyr Thr Met Asn Pro Asn Lys Phe Arg Ala Cys
    530                 535                 540

Gln Phe Leu Ile Lys Phe His Glu Arg Arg Asn Asp Lys Ile Ile Val
545                 550                 555                 560

Phe Ala Asp Asn Val Phe Ala Leu Lys Glu Tyr Ala Ile Arg Leu Asn
                565                 570                 575

Lys Pro Tyr Ile Tyr Gly Pro Thr Ser Gln Gly Glu Arg Met Gln Ile
            580                 585                 590
```

```
Leu Gln Asn Phe Lys His Asn Pro Lys Ile Asn Thr Ile Phe Ile Ser
        595                 600                 605

Lys Val Gly Asp Thr Ser Phe Asp Leu Pro Glu Ala Asn Val Leu Ile
    610                 615                 620

Gln Ile Ser Ser His Gly Gly Ser Arg Arg Gln Glu Ala Gln Arg Leu
625                 630                 635                 640

Gly Arg Val Leu Arg Ala Lys Lys Gly Met Val Ala Glu Glu Tyr Asn
                645                 650                 655

Ala Phe Phe Tyr Ser Leu Val Ser Gln Asp Thr Gln Glu Met Ala Tyr
            660                 665                 670

Ser Thr Lys Arg Gln Arg Phe Leu Val Gln Gly Tyr Ser Phe Lys Val
        675                 680                 685

Ile Thr Lys Leu Ala Gly Met Glu Glu Glu Asp Leu Ala Phe Ser Thr
    690                 695                 700

Lys Glu Glu Gln Gln Gln Leu Leu Gln Lys Val Leu Ala Ala Thr Asp
705                 710                 715                 720

Leu Asp Ala Glu Glu Glu Val Val Ala Gly Glu Phe Gly Ser Arg Ser
                725                 730                 735

Ser Gln Ala Ser Arg Arg Phe Gly Thr Met Ser Ser Met Ser Gly Ala
            740                 745                 750

Asp Asp Thr Val Tyr Met Glu Tyr His Ser Ser Arg Ser Lys Ala Pro
        755                 760                 765

Ser Lys His Val His Pro Leu Phe Lys Arg Phe Arg Lys
    770                 775                 780
```

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..15
(D) OTHER INFORMATION: /note= "Peptide # 464: XPB peptide that binds wild-type p53 protein."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
Leu Gly Leu Thr Ala Thr Leu Val Arg Glu Asp Asp Lys Ile Val
1               5                   10                  15
```

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..15
(D) OTHER INFORMATION: /note= "Peptide # 479: XPB peptide that does not bind wild-type p53 protein."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Asp Leu Asn Phe Leu Ile Gly Pro Lys Leu Tyr Glu Ala Asn Trp
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..16
(D) OTHER INFORMATION: /note= "Peptide # 99: control peptide."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Gly Leu Ser Ala Met Ser Thr Thr Asp Leu Glu Ala Tyr Phe Lys Asp
1 5 10 15